



SEQUENCE LISTING

<110> Lead B.V.
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DAMEN-VAN OORSCHOT, Astrid Adriana Anna Maria

<120> MOLECULES INTERACTING WITH APOPTIN

<130> 2906-5008

<140> 09/551981

<141> 2000-06-26

<150> PCT/NL98/00687

<151> 1998-12-03

<150> EP 97203781.6

<151> 1997-12-12

<160> 17

<170> PatentIn version 3.0

<210> 1

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<221> misc_feature

<223> pACT-specific sequencing primer

<400> 1

taccactaca atggatg

17

<210> 2

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<221> misc_feature

<223> Hou/Nmi-like protein putative immunogenic peptide

<400> 2

Arg Asn Gly Gly Gly Glu Val Asp Arg Val Asp Tyr Asp Arg Gln
1 5 10 15

<210> 3

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<221> misc_feature

<223> IFP35-like protein putative immunogenic peptide

<400> 3

Cys Gln Leu Arg Lys Glu Leu Gly Asp Ser Pro Lys Asp Lys Val Pro
1 5 10 15

<210> 4

<211> 658

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(658)

<223> for any n in the sequence, n is an undefined base

<400> 4

gggggatcat ggaagctgat aaagatgaca cacaacaaat tcttaaggag cattcgccag 60

atgaatttat aaaagatgaa caaaaataagg gactaattga tgaaattaca aagaaaaata 120

ttcaactaaa gaaggagatc caaaagcttg aaacggagtt acaagaggct accaaagaat 180

tccagattaa agaggatatt cctgaaacaa agatgaaatt cttatcgtt gaaactcctg 240

agaatgacag ccagttgtca aatatctcct gttcggttca agttagctcg aaagttcctt 300

atgagataca aaaaggacaa gcacttatca cctttgaaaa agaagaagtt gctcaaaatg 360

tggtaagcat gagtaaacat catgtacaga taaaagatgt aaatctggag gttacggcca 420

agccagttcc attaaattca ggagtcagat tccaggttta tgtagaagtt tctaaaatga 480

aaatcaatgt tactgaaatt cctgacacat tgcgtgaaga tcaaattgaga gacaaactag 540

agctgagctt ttcaaagtcc cgaaatggg ggcggagang tggaccgcgt gggactatga 600

cagacagtcc gggagtgcag tcacacgtt tggngagat tggagtgcc tgacannn 658

<210> 5

<211> 719

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(719)

<223> for any n in the sequence, n is an undefined base

<400> 5

cgaggattaca agaggctacc aaagaattcc agattaaaga ggatattcct gaaacaaaga 60

tgaaattctt atcagttgaa actcctgana atgacagcca gttgtcaaatt atctcctgtt 120

cgttcaagg tgagctgaa agttcctt atgatcacaa aaggacaatg cacttatcac 180

cttgaaaaa ggaagaagtt gctcaaaatg tgnntaangc atgatcaaac atcatgtaca 240

gataataaga tgtaaatctg gaggttacgg ccaaagccaa gttccattaa tattcaagga 300

gtcangattc cagngtttat gctagaangt ttctaaaaat ganaatcaat ggtaactgga	360
aattcctgga cacattgcgn tggaaagatca agatgacgaa gacaaactaa gaagctgagc	420
ttttcaaaag tcccgaaana tggaagagcg gtagagggtg gnaccgcgtg nganctatga	480
caagacaagn ccggggaagn tgcaagtccat cacgttgtt ngaagattgg angtnggctg	540
accaangaat tttgaaaaag gagangaatt acccctctt angagtaana tcaaaaccct	600
gccataanaa gtnactggt ttcncccatt acacagnant tacannttga ncaanantan	660
ncaggataat ttncagggga anaatctnaa gnatggcaag ntgacttctg gacaanggt	719

<210> 6
<211> 220
<212> PRT
<213> Homo sapiens

<400> 6

His Glu Gly Arg Gly Ile Met Glu Ala Asp Lys Asp Asp Thr Gln Gln			
1	5	10	15
10	15		

Ile Leu Lys Glu His Ser Pro Asp Glu Phe Ile Lys Asp Glu Gln Asn			
20	25	30	
30			

Lys Gly Leu Ile Asp Glu Ile Thr Lys Lys Asn Ile Gln Leu Lys Lys			
35	40	45	
45			

Glu Ile Gln Lys Leu Glu Thr Glu Leu Gln Glu Ala Thr Lys Glu Phe			
50	55	60	
60			

Gln Ile Lys Glu Asp Ile Pro Glu Thr Lys Met Lys Phe Leu Ser Val			
65	70	75	80
75	80		

Glu Thr Pro Glu Asn Asp Ser Gln Leu Ser Asp Ile Ser Cys Ser Phe			
85	90	95	
95			

Gln Val Ser Ser Lys Val Pro Thr Glu Ile Gln Lys Gly Gln Ala Leu			
100	105	110	
110			

Ile Thr Phe Glu Lys Glu Glu Val Ala Gln Asn Val Val Ser Met Ser			
115	120	125	
125			

Lys His His Val Gln Ile Lys Asp Val Asn Leu Glu Val Thr Ala Lys			
130	135	140	
140			

Pro Val Pro Leu Asn Ser Gly Val Arg Phe Gln Val Thr Val Glu Val			
145	150	155	160
155	160		

Ser Lys Met Lys Ile Asn Val Thr Glu Ile Pro Asp Thr Leu Arg Glu			
165	170	175	
175			

Asp Gln Met Arg Arg Lys Leu Glu Leu Ser Phe Ser Lys Ser Arg Asn			
180	185	190	
190			

Gly Arg Arg Arg Cys Gly Pro Arg Gly Thr Met Thr Asp Ser Pro Gly
 195 200 205
 Val Gln Ser Ser Arg Leu Val Glu Ile Gly Ser Gly
 210 215 220
 <210> 7
 <211> 307
 <212> PRT
 <213> Homo sapiens
 <400> 7
 Met Glu Ala Asp Lys Asp Asp Thr Gln Gln Ile Leu Lys Glu His Ser
 1 5 10 15
 Pro Asp Glu Phe Ile Lys Asp Glu Gln Asn Lys Gly Leu Ile Asp Glu
 20 25 30
 Ile Thr Lys Lys Asn Ile Gln Leu Lys Lys Glu Ile Gln Lys Leu Glu
 35 40 45
 Thr Glu Leu Gln Glu Ala Thr Lys Glu Phe Gln Ile Lys Glu Asp Ile
 50 55 60
 Pro Glu Thr Lys Met Lys Phe Leu Ser Val Glu Thr Pro Glu Asn Asp
 65 70 75 80
 Ser Gln Leu Ser Asn Ile Ser Cys Ser Phe Gln Val Ser Ser Lys Val
 85 90 95
 Pro Tyr Glu Ile Gln Lys Gly Gln Ala Leu Ile Thr Phe Glu Lys Glu
 100 105 110
 Glu Val Ala Gln Asn Val Val Ser Met Ser Lys His His Val Gln Ile
 115 120 125
 Lys Asp Val Asn Leu Glu Val Thr Ala Lys Pro Val Pro Leu Asn Ser
 130 135 140
 Gly Val Arg Phe Gln Val Thr Val Glu Val Ser Lys Met Lys Ile Asn
 145 150 155 160
 Val Thr Glu Ile Pro Asp Thr Leu Lys Glu Asp Gln Met Arg Asp Lys
 165 170 175
 Leu Glu Leu Ser Phe Ser Lys Phe Arg Asn Gly Gly Glu Val Asp
 180 185 190
 Arg Val Asp Tyr Asp Arg Gln Ser Gly Ser Ala Val Ile Thr Phe Val
 195 200 205
 Glu Ile Gly Val Ala Asp Lys Ile Leu Lys Lys Glu Tyr Pro Leu
 210 215 220
 Tyr Ile Asn Gln Thr Cys His Arg Val Thr Val Ser Pro Tyr Thr Glu
 225 230 235 240
 Ile His Leu Lys Lys Tyr Gln Ile Phe Ser Gly Thr Ser Lys Arg Thr

245	250	255
Val Leu Leu Thr Gly Met Glu Gly Ile Gln Met Asp Glu Glu Ile Val		
260	265	270
Glu Asp Leu Ile Asn Ile His Phe Gln Arg Ala Lys Asn Gly Gly Gly		
275	280	285
Glu Val Asp Val Val Lys Cys Ser Leu Gly Gln Pro His Ile Ala Tyr		
290	295	300
Phe Glu Glu		
305		
<210> 8		
<211> 659		
<212> DNA		
<213> Homo sapiens		
<220>		
<221> misc_feature		
<222> (1)...(659)		
<223> for any n in the sequence, n is an undefined base		
<400> 8		
agcagggtgct gcaacaaaag gagcacacga tcaacatgga ggagtgccgg ctgcgggtgc	60	
aggtcagcc cttggagctg cccatggtca ccaccatcca ggtgtccagc cagttgagtg	120	
gccggagggt gttggtaact ggatttcctg ccagcctcag gctgagtgag gaggagctgc	180	
tggacaanct anagatcttc ttggcaaga ctagaacgg aggtggcnat gtggacnttc	240	
ggganctact gccagggant gtcatgctgg ggtttgctag ggatggagtg gctcancgtc	300	
tgtgccaaat cggccatttc acagtgccac tgggtggca gcangccct ctgagagtct	360	
ctccgtatgt gaatggggan atccagangg ctganatcag gtcncagcca ntccccgct	420	
cggtaactggt gctcaacatt cctgatatct tggatggccc ggagctgcat gacgtcctgg	480	
anatccactt ccagaanccc acccgcgggg gcggagatgt aagacgccct gacagtcgta	540	
ccccaaggac aacagggcct aacagtcttc acctcctgaa tcaaggctan gggcctcccc	600	
cttctcatcc tccccacccc ccccgccaaa ggttctcaan actgggcctg ggcttntg	659	

<210> 9		
<211> 630		
<212> DNA		
<213> Homo sapiens		
<220>		
<221> misc_feature		
<222> (1)...(630)		
<223> for any n in the sequence, n is an undefined base		

<400> 9	
ccaaagtggc tgagcaggtg ctgcaacaaa aggagcacac gatcaacatg gaggagtgcc	60
ggctgcgggt gcaggtccag cccttggagc tgcccattgtt caccaccatc caggtgtcca	120
gccagtttag tggccggagg gtgttgtca ctggatttcc tgccagcctc aggctgagtg	180
aggagggact gctggacaag cttagagatot tctttggcaa gacttaggaac ggaggtggcg	240
atgtggacgt tcgggagcta ctgccaggga gtgtcatgct ggggtttgct agggatggag	300
tggctcagcg tctgtgccaa atcggccaag ttcacagtgc cactgggtgg gcancaagtc	360
cctctgagag tctctccgta tgtgaatggg gagatccaga aggctgagat caggtcgcan	420
ccagttcccc nctcggtact ggggtctcaa cattcctgat atcttggatt ggcccgagc	480
tgcacnacgt cctgganatc aacttcanaa gcccacccgc cggggcngng aggtanaagg	540
cctgacatcn ttacccaaa ggacagcatg gncctaacad tcctcacctc cnaatcangc	600
tnnggggctn cccttctanc ntcccaactg	630

<210> 10
 <211> 631
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(631)
 <223> for any n in the sequence, n is an undefined base

<400> 10	
ggatccactg ccctctgctt gcgggctctg ctctgatcac ctttgatgac cccaaagtgg	60
ctgagcaggt gctgcaacaa aaggagcaca cgatcaacat ggaggagtgc cggctgcggg	120
tgcaggtcca gcccttggag ctgcccattgg tcaccaccat ccaggtgtatg gtgtccagcc	180
anttgagtgg ccggaggggtg ttggtcactg gatttcctgc cagcctcagg ctgantgagg	240
aggagctgct ggacaagcta tgagatcttc tttggcaana ctangaacgg angtggcgat	300
gtggacgttc gggagctact gccagggagt gtcatgctgg gtttgctac ggatggagtg	360
gctcagcgtc tgtgccaaat cgccagttc acaagtgcc a ctgggtggc agcaagtccc	420
tctgagagtc tctccgtatg tgantggnga gatcagaatg ctganattaa gtcgcaccca	480
attcctcgct cnggtactgg tgctcannat cctganatct tggattggcc ccngantnca	540
tganatctgg nagattcaat tncanaagtc canccnnncng ngncgggaag tanangcccg	600
ananttcntn ncntanggnnc agcanngcct g	631

<210> 11

<211> 138
<212> PRT
<213> Homo sapiens

<400> 11

His Glu Gly Pro Lys Val Ala Glu Gln Val Leu Gln Gln Lys Glu His
1 5 10 15

Thr Ile Asn Met Glu Glu Cys Arg Leu Arg Val Gln Val Gln Pro Leu
20 25 30

Glu Leu Pro Met Val Thr Thr Ile Gln Val Ser Ser Gln Leu Ser Gly
35 40 45

Arg Arg Val Leu Val Thr Gly Phe Pro Ala Ser Leu Arg Leu Ser Glu
50 55 60

Glu Glu Leu Leu Asp Lys Leu Glu Ile Phe Phe Gly Lys Thr Arg Asn
65 70 75 80

Gly Gly Gly Asp Val Asp Val Arg Glu Leu Leu Pro Gly Ser Val Met
85 90 95

Leu Gly Phe Ala Arg Asp Gly Val Ala Gln Arg Leu Cys Gln Ile Gly
100 105 110

Gln Val His Ser Ala Thr Gly Trp Ala Ser Ser Pro Ser Glu Ser Leu
115 120 125

Ser Val Cys Glu Trp Gly Asp Pro Glu Gly
130 135

<210> 12
<211> 282
<212> PRT
<213> Homo sapiens

<400> 12

Met Ser Ala Pro Leu Asp Ala Ala Leu His Ala Leu Gln Glu Glu Gln
1 5 10 15

Ala Arg Leu Lys Met Arg Leu Trp Asp Leu Gln Gln Leu Arg Lys Glu
20 25 30

Leu Gly Asp Ser Pro Lys Asp Lys Val Pro Phe Ser Val Pro Lys Ile
35 40 45

Pro Leu Val Phe Arg Gly His Thr Gln Gln Asp Pro Glu Val Pro Lys
50 55 60

Ser Leu Val Ser Asn Leu Arg Ile His Cys Pro Leu Leu Ala Gly Ser
65 70 75 80

Ala Leu Ile Thr Phe Asp Asp Pro Lys Val Ala Glu Gln Val Leu Gln
85 90 95

Gln Lys Glu His Thr Ile Asn Met Glu Glu Cys Arg Leu Arg Val Gln

100	105	110	
Val Gln Pro Leu Glu Leu Pro Met Val Thr Thr Ile Gln Val Ser Ser			
115	120	125	
Gln Leu Ser Gly Arg Arg Val Leu Val Thr Gly Phe Pro Ala Ser Leu			
130	135	140	
Arg Leu Ser Glu Glu Leu Leu Asp Lys Leu Glu Ile Phe Phe Gly			
145	150	155	160
Lys Thr Arg Asn Gly Gly Asp Val Asp Val Arg Glu Leu Leu Pro			
165	170	175	
Gly Ser Val Met Leu Gly Phe Ala Arg Asp Gly Val Ala Gln Arg Leu			
180	185	190	
Cys Gln Ile Gly Gln Phe Thr Val Pro Leu Gly Gly Gln Gln Val Pro			
195	200	205	
Leu Arg Val Ser Pro Tyr Val Asn Gly Glu Ile Gln Lys Ala Glu Ile			
210	215	220	
Arg Ser Gln Pro Val Pro Arg Ser Val Leu Val Leu Asn Ile Pro Asp			
225	230	235	240
Ile Leu Asp Gly Pro Glu Leu His Asp Val Leu Glu Ile His Phe Gln			
245	250	255	
Lys Pro Thr Arg Gly Gly Gly Arg Gly Pro Asp Ser Arg Thr Pro			
260	265	270	
Arg Thr Ala Gly Pro Ser Ser Leu His Leu			
275	280		
<210> 13			
<211> 207			
<212> PRT			
<213> Homo sapiens			
<220>			
<221> misc_feature			
<222> (1)...(207)			
<223> for any Xaa in the sequence, Xaa is an undefined amino acid			
<400> 13			
His Glu Gly Arg Ile His Cys Pro Leu Leu Ala Gly Ser Ala Leu Ile			
1	5	10	15
Thr Phe Asp Asp Pro Lys Val Ala Glu Gln Val Leu Gln Lys Glu			
20	25	30	
His Thr Ile Asn Met Glu Glu Cys Arg Leu Arg Val Gln Val Gln Pro			
35	40	45	
Leu Glu Leu Pro Met Val Thr Thr Ile Gln Val Met Val Ser Ser Xaa			
50	55	60	

Leu Ser Gly Arg Arg Val Leu Val Thr Gly Phe Pro Ala Ser Leu Arg
 65 70 75 80

 Leu Xaa Glu Glu Glu Leu Leu Asp Lys Leu Asp Leu Leu Trp Gln Xaa
 85 90 95

 Xaa Glu Arg Xaa Trp Arg Cys Gly Arg Ser Gly Ala Thr Ala Arg Glu
 100 105 110

 Cys His Ala Gly Val Cys Tyr Gly Trp Ser Gly Ser Ala Ser Val Pro
 115 120 125

 Asn Arg Pro Val His Lys Cys His Trp Val Gly Ser Lys Ser Leu Glu
 130 135 140

 Ser Leu Arg Met Xaa Xaa Arg Ser Glu Cys Xaa Val Ala Ser Asn Ser
 145 150 155 160

 Ser Leu Xaa Tyr Trp Cys Ser Xaa Ser Xaa Leu Gly Leu Ala Pro Xaa
 165 170 175

 Xaa Met Xaa Ser Gly Arg Phe Asn Xaa Xaa Ser Pro Xaa Xaa Xaa Xaa
 180 185 190

 Gly Lys Xaa Xaa Pro Xaa Xaa Ser Xaa Xaa Xaa Xaa Ser Xaa Ala
 195 200 205

 <210> 14
 <211> 647
 <212> PRT

 <213> Homo sapiens

 <400> 14

 Arg Leu Arg Asn Gly His Val Gly Ile Ser Phe Val Pro Lys Glu Thr
 1 5 10 15

 Gly Glu His Leu Val His Val Lys Lys Asn Gly Gln His Val Ala Ser
 20 25 30

 Ser Pro Ile Pro Val Val Ile Ser Gln Ser Glu Ile Gly Asp Ala Ser
 35 40 45

 Arg Val Arg Val Ser Gly Gln Gly Leu His Glu Gly His Thr Phe Glu
 50 55 60

 Pro Ala Glu Phe Ile Ile Asp Thr Arg Asp Ala Gly Tyr Gly Leu
 65 70 75 80

 Ser Leu Ser Ile Glu Gly Pro Ser Lys Val Asp Ile Asn Thr Glu Asp
 85 90 95

 Leu Glu Asp Gly Thr Cys Arg Val Thr Tyr Cys Pro Thr Glu Pro Gly
 100 105 110

 Asn Tyr Ile Ile Asn Ile Lys Phe Ala Asp Gln His Val Pro Gly Ser
 115 120 125

Pro Phe Ser Val Lys Val Thr Gly Glu Gly Arg Val Lys Glu Ser Ile
 130 135 140
 Thr Arg Arg Arg Ala Pro Ser Val Ala Asn Val Gly Ser His Cys
 145 150 155 160
 Asp Leu Ser Leu Lys Ile Pro Glu Ile Ser Ile Gln Asp Met Thr Ala
 165 170 175
 Gln Val Thr Ser Pro Ser Gly Lys Thr His Glu Ala Glu Ile Val Glu
 180 185 190
 Gly Glu Asn His Thr Tyr Cys Ile Arg Phe Val Pro Ala Glu Met Gly
 195 200 205
 Thr His Thr Val Ser Val Lys Tyr Lys Gly Gln His Val Pro Gly Ser
 210 215 220
 Pro Phe Gln Phe Thr Val Gly Pro Leu Gly Glu Gly Ala His Lys
 225 230 235 240
 Val Arg Ala Gly Gly Pro Gly Leu Glu Arg Ala Glu Ala Gly Val Pro
 245 250 255
 Ala Glu Phe Ser Ile Trp Thr Arg Glu Ala Gly Ala Gly Leu Ala
 260 265 270
 Ile Ala Val Glu Gly Pro Ser Lys Ala Glu Ile Ser Phe Glu Asp Arg
 275 280 285
 Lys Asp Gly Ser Cys Gly Val Ala Tyr Val Val Gln Glu Pro Gly Asp
 290 295 300
 Tyr Glu Val Ser Val Lys Phe Asn Glu Glu His Ile Pro Asp Ser Pro
 305 310 315 320
 Phe Val Val Pro Val Ala Ser Pro Ser Gly Asp Ala Arg Arg Leu Thr
 325 330 335
 Val Ser Ser Leu Gln Glu Ser Gly Leu Lys Val Asn Gln Pro Ala Ser
 340 345 350
 Phe Ala Val Ser Leu Asn Gly Ala Lys Gly Ala Ile Asp Ala Lys Val
 355 360 365
 His Ser Pro Ser Gly Ala Leu Glu Glu Cys Tyr Val Thr Glu Ile Asp
 370 375 380
 Gln Asp Lys Tyr Ala Val Arg Phe Ile Pro Arg Glu Asn Gly Val Tyr
 385 390 395 400
 Leu Ile Asp Val Lys Phe Asn Gly Thr His Ile Pro Gly Ser Pro Phe
 405 410 415
 Lys Ile Arg Val Gly Glu Pro Gly His Gly Gly Asp Pro Gly Leu Val
 420 425 430
 Ser Ala Tyr Gly Ala Gly Leu Glu Gly Val Thr Gly Asn Pro Ala
 435 440 445

Glu Phe Val Val Asn Thr Ser Asn Ala Gly Ala Gly Ala Leu Ser Val
 450 455 460
 Thr Ile Asp Gly Pro Ser Lys Val Lys Met Asp Cys Gln Glu Cys Pro
 465 470 475 480
 Glu Gly Tyr Arg Val Thr Tyr Thr Pro Met Ala Pro Gly Ser Tyr Leu
 485 490 495
 Ile Ser Ile Lys Tyr Gly Gly Pro Tyr His Ile Gly Gly Ser Pro Phe
 500 505 510
 Lys Ala Lys Val Thr Gly Pro Arg Leu Val Ser Asn His Ser Leu His
 515 520 525
 Glu Thr Ser Ser Val Phe Val Asp Ser Leu Thr Lys Ala Thr Cys Ala
 530 535 540
 Pro Gln His Gly Ala Pro Gly Pro Gly Pro Ala Asp Ala Ser Lys Val
 545 550 555 560
 Val Ala Lys Gly Leu Gly Leu Ser Lys Ala Tyr Val Gly Gln Lys Ser
 565 570 575
 Ser Phe Thr Val Asp Cys Ser Lys Ala Gly Asn Asn Met Leu Leu Val
 580 585 590
 Gly Val His Gly Pro Arg Thr Pro Cys Glu Glu Ile Leu Val Lys His
 595 600 605
 Val Gly Ser Arg Leu Tyr Ser Val Ser Tyr Leu Leu Lys Asp Lys Gly
 610 615 620
 Glu Tyr Thr Leu Val Val Lys Trp Gly His Glu His Ile Pro Gly Ser
 625 630 635 640
 Pro Tyr Arg Val Val Val Pro
 645
 <210> 15
 <211> 213
 <212> PRT
 <213> Homo sapiens
 <400> 15
 His Glu Gly Arg Gly Val Thr Gly Asn Pro Ala Glu Phe Val Val Asn
 1 5 10 15
 Thr Ser Asn Ala Gly Ala Gly Ala Leu Ser Val Thr Ile Asp Gly Pro
 20 25 30
 Ser Lys Val Lys Met Asp Cys Gln Glu Cys Pro Glu Gly Tyr Arg Val
 35 40 45
 Thr Tyr Thr Pro Met Ala Pro Gly Ser Tyr Leu Ile Ser Ile Lys Tyr
 50 55 60

Gly Gly Pro Tyr His Ile Gly Gly Ser Pro Phe Lys Ala Lys Val Thr
 65 70 75 80

Gly Pro Arg Leu Val Ser Asn His Ser Leu His Glu Thr Ser Ser Val
 85 90 95

Phe Val Asp Ser Leu Thr Lys Ala Thr Cys Ala Pro His His Gly Ala
 100 105 110

Pro Gly Pro Gly Pro Ala Asp Ala Ser Lys Val Val Ala Lys Gly Leu
 115 120 125

Gly Leu Ser Lys Ala Tyr Val Cys His Lys Ser Ser Phe Thr Val Asp
 130 135 140

Cys Ser Lys Ala Cys Ile Ile Met Leu Leu Val Gly Val His Gly Pro
 145 150 155 160

Trp Thr Pro Cys Asp Glu Ile Leu Val Lys Ala Arg Gly Gln Pro Ala
 165 170 175

Leu Gln Arg Val Leu Thr Cys Phe Lys Asp Lys Gly Glu Val His Thr
 180 185 190

Gly Gly Gln Asn Gly Gly Asp Tyr Gln Ile Pro Cys Lys Pro Leu Pro
 195 200 205

Leu Cys Gly Cys Pro
 210

<210> 16
 <211> 213
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(213)
 <223> for any Xaa in the sequence, Xaa is an undefined amino acid

<400> 16

His Glu Gly Arg Pro Thr Glu Pro Gly Asn Tyr Ile Ile Asn Ile Lys
 1 5 10 15

Phe Ala Asp Gln His Val Pro Gly Ser Pro Phe Ser Val Lys Val Thr
 20 25 30

Gly Glu Gly Arg Val Lys Glu Ser Ile Thr Arg Arg Arg Ala Pro
 35 40 45

Ser Val Ala Asn Val Gly Ser His Cys Asp Leu Ser Leu Lys Ile Pro
 50 55 60

Glu Ile Ser Ile Gln Asp Met Thr Ala Gln Val Thr Ser Pro Ser Gly
 65 70 75 80

Lys Thr His Glu Ala Glu Ile Val Glu Gly Glu Asn His Thr Tyr Cys
 85 90 95

Ile Arg Phe Val Pro Ala Glu Met Gly Thr His Thr Val Ser Val Lys
100 105 110

Tyr Lys Gly Gln His Val Pro Gly Ser Pro Phe Gln Phe Thr Val Gly
115 120 125

Pro Leu Gly Glu Gly Gly Ala His Xaa Val Arg Ala Gly Gly Pro Gly
130 135 140

Leu Xaa Lys Ser Ser Trp Ser Ala Ser Arg Ile Gln Tyr Leu Gly Pro
145 150 155 160

Gly Lys Leu Val Leu Glu Ala Trp Pro Leu Leu Ser Xaa Ala Pro Ala
165 170 175

Xaa Leu Xaa Ser Leu Leu Arg Thr Ala Arg Thr Ala Pro Val Val Leu
180 185 190

Leu Met Leu Val Xaa Glu Pro Ser Asp Xaa Asn Pro Xaa Gln Val Ser
195 200 205

Thr Lys Glu His Xaa
210

<210> 17
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> misc_feature
<223> Myc-tag peptide

<400> 17

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
1 5 10